16.   A method for identifying polymorphic markers in a population, comprising the steps of:

characterizing a first sample that includes a plurality of individuals from the population;

providing a representative genomic DNA microarray;

selecting an individual from the first sample;

hybridizing genomic DNA of the selected individual with the representative microarray;

determining segments of hybridization between the genomic DNA of the selected

individual and the representative microarray;

calculating a hybridization intensity ratio for each hybridized segment;

converting each intensity ratio into a numerical element;

compiling data consisting of the numerical elements; and

analyzing the data to identify patterns of hybridization present in the population.

17.   The method of claim 16, wherein the representative microarray is fabricated from genomic DNA from an individual in the population.

18.   The method of claim 16, wherein the step of selecting an individual from the first sample involves selecting an individual that shares the most characteristics among other individuals of the same population.

19.   The method of claim 16, further comprising the step of hybridizing genomic DNA from each of the individuals in the first sample to the representative microarray to determine genetic relatedness of the individuals from the first sample.

20.   The method of claim 16, further comprising the steps of:

characterizing a second sample that includes a plurality of selected individuals from the

same population;

hybridizing genomic DNA from each of the selected individuals in the second sample to

the representative microarray to determine genetic relatedness of the individuals in the

population.

21.   The method of claim 20, wherein at least one of the first and second samples is characterized by genotype, and at least one of the individuals selected from the first and second samples is selected based upon the genotypic characterization.

22.   The method of claim 20, wherein at least one of the first and second samples is characterized by phenotype, and at least one of the individuals selected from the first and second samples is selected based upon the phenotypic characterization.

23.   The method of claim 18, further comprising the step of labeling the genomic DNA of each selected individual with a fluorescent dye.

24.   The method of claim 23, wherein the genomic DNA of each selected individual is labeled with a different fluorescent dye.

25.   The method of claim 23, wherein the step of determining each segment's hybridization intensity includes determining the fluorescent intensities of the hybridized segments.

26.   The method of claim 16, wherein the numerical element is an integer.

27.   The method of claim 16, wherein the step of converting includes binary conversion, and the numerical element is a binary digit consisting of a 0 or 1 bit.

28.   The method of claim 27, wherein the step of compiling data produces a string of binary bits corresponding to the selected individual in the sample.

29.   The method of claim 28, further including the step of collecting the bit string for each individual in the sample into a composite file.

30.   The method of claim 29, wherein the step of analyzing further includes normalizing the data through mean and median centering of each of the hybridization intensity ratios.

31.   The method of claim 29, further including the step of preparing a graphical representation for each bit string.

32.   The method of claim 16, wherein the population is a bacterial population.

33.   The method of claim 32, wherein the bacterial population is selected from the group consisting of *Listeria monocytogenes, Escherichia coli, Lactobacillus casei, Lactobacillus lactus, Salmonella typhimurium, Salmonella entereditis*, and *Salmonella typhi*.

34.   A method for identifying polymorphic markers in a bacterial population comprising a plurality of individuals, involving the steps of:

        providing a plurality of bit strings, each string representing an individual within the population and having the same number and position of bits, each bit having a value of 0 or 1;

        generating a graphical representation of the relatedness of the bit strings, the graphical representation including selectable elements;

        selecting a first selectable element;

        selecting a second selectable element; and

        identifying bits that are present in each bit string representing the first selectable element and absent in each bit string representing the second selectable element, or bits that are absent in each bit string representing the first selectable element and present in each bit string representing the second selectable element.

35.   The method of claim 34, wherein the relatedness of the bit strings is determined by the commonality of bit values at corresponding positions in the bit strings.

36.   The method of claim 34, wherein the graphical representation is a dendrogram and the selectable elements are leaves and nodes, each leaf representing a single bit string, and each node representing two or more bit strings.